

#15

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RAW SEQUENCE LISTING

DATE: 03/18/2003

PATENT APPLICATION: US/09/754,032

TIME: 10:37:16

Input Set : N:\Cr3\RULE60\09754032.RAW.txt

Output Set: N:\CRF4\03182003\I754032.raw

SEQUENCE LISTING

```

3 (1) GENERAL INFORMATION:
5   (i) APPLICANT: SCOTT, MATHEW P
6       GOODRICH, LISA V
7       JOHNSON, RONALD L
9   (ii) TITLE OF INVENTION: Patched Genes and their Use
11  (iii) NUMBER OF SEQUENCES: 19
13  (iv) CORRESPONDENCE ADDRESS:
14      (A) ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
15      (B) STREET: Four Embarcadero Center, Suite 3400
16      (C) CITY: San Francisco
17      (D) STATE: CA
18      (E) COUNTRY: US
19      (F) ZIP: 94111
21  (v) COMPUTER READABLE FORM:
22      (A) MEDIUM TYPE: Floppy disk
23      (B) COMPUTER: IBM PC compatible
24      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25      (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27  (vi) CURRENT APPLICATION DATA:
C--> 28      (A) APPLICATION NUMBER: US/09/754,032
C--> 29      (B) FILING DATE: 03-Jan-2001
W--> 34      (C) CLASSIFICATION: 435
31  (vii) PRIOR APPLICATION DATA:
32      (A) APPLICATION NUMBER: US/08/540,406
33      (B) FILING DATE: 06-OCT-1995
35  (viii) ATTORNEY/AGENT INFORMATION:
36      (A) NAME: Rowland, Bertram I
37      (B) REGISTRATION NUMBER: 20015
38      (C) REFERENCE/DOCKET NUMBER: a60190-1
40  (ix) TELECOMMUNICATION INFORMATION:
41      (A) TELEPHONE: 415-781-1989
42      (B) TELEFAX: 415-398-3249
45 (2) INFORMATION FOR SEQ ID NO: 1:
47   (i) SEQUENCE CHARACTERISTICS:
48      (A) LENGTH: 736 base pairs
49      (B) TYPE: nucleic acid
50      (C) STRANDEDNESS: single
51      (D) TOPOLOGY: linear
53   (ii) MOLECULE TYPE: DNA (genomic)
58   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
60 AACNNCNTNT NATGGCACCC CCNCCCAACC TTTNNNCCNN NTAANCAAAA NNCCCCNTTT      60
62 NATACCCCT NTAANANTTT TCCACCNNNC NNAAANNCCN CTGNANACNA NGNAAANCCN      120

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64 TTTTNAACC CCCCCACCC GGAATTCNA NTNNCCNCCC CCAAATTACA ACTCCAGNCC 180
66 AAAATTNANA NAATTGGTCC TAACCTAACC NATNGTTGTT ACGGTTTCCC CCCCCAAATA 240
68 CATGCACTGG CCCGAACACT TGATCGTTGC CGTTCCAATA AGAATAAATC TGGTCATATT 300
70 AAACAAGCCN AAAGCTTTAC AAAGTGTGT ACAATTAATG GGCGAACACG AACTGTTCTGA 360
72 ATTCTGGTCT GGACATTACA AAGTGCACCA CATCGGATGG AACCAGGAGA AGGCCACAAC 420
74 CGTACTGAAC GCCTGGCAGA AGAAGTTCGC ACAGGTTGGT GGTGGCGCA AGGAGTAGAG 480
76 TGAATGGTGG TAATTTTTGG TTGTTCCAGG AGGTGGATCG TCTGACGAAG AGCAAGAAGT 540
78 CGTCGAATTA CATCTTCGTG ACGTTCCTCA CCGCCAATTT GAACAAGATG TTGAAGGAGG 600
80 CGTCGAANAC GGACGTGGTG AAGCTGGGGG TGGTGGCTGG GGTGGCGCGG GTGTACGGGT 660
82 GGGTGGCCCA GTCGGGGCTG GCTGCCTTGG GAGTGTGGT CTTNGCGNGC TNCNATTCGC 720
84 CCTATAGTNA GNCGTA 736

```

86 (2) INFORMATION FOR SEQ ID NO: 2:

88 (i) SEQUENCE CHARACTERISTICS:

89 (A) LENGTH: 107 amino acids

90 (B) TYPE: amino acid

91 (C) STRANDEDNESS: single

92 (D) TOPOLOGY: linear

94 (ii) MOLECULE TYPE: protein

99 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

W--> 101 Xaa Pro Pro Pro Asn Tyr Asn Ser Xaa Pro Lys Xaa Xaa Xaa Leu Val
102 1 5 10 15
104 Leu Thr Pro Xaa Val Val Thr Val Ser Pro Pro Lys Tyr Met His Trp
105 20 25 30
107 Pro Glu His Leu Ile Val Ala Val Pro Ile Arg Ile Asn Leu Val Ile
108 35 40 45
110 Leu Asn Lys Pro Lys Ala Leu Gln Thr Val Val Gln Leu Met Gly Glu
111 50 55 60
113 His Glu Leu Phe Glu Phe Trp Ser Gly His Tyr Lys Val His His Ile
114 65 70 75 80
116 Gly Trp Asn Gln Glu Lys Ala Thr Thr Val Leu Asn Ala Trp Gln Lys
117 85 90 95
119 Lys Phe Ala Gln Val Gly Gly Trp Arg Lys Glu
120 100 105

```

122 (2) INFORMATION FOR SEQ ID NO: 3:

124 (i) SEQUENCE CHARACTERISTICS:

125 (A) LENGTH: 5187 base pairs

126 (B) TYPE: nucleic acid

127 (C) STRANDEDNESS: single

128 (D) TOPOLOGY: linear

130 (ii) MOLECULE TYPE: cDNA

135 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

137 GGGTCTGTCA CCCGAGCCG GAGTCCCCG CGGCCAGCAG CGTCCTCGCG AGCCGAGCGC 60
139 CCAGGCGCGC CCGGAGCCCG CGGCGGCGCG GGCAACATGG CCTCGGCTGG TAACGCCGCC 120
141 GGGGCCCTGG GCAGGACGGC CGGCGGCGGG AGGCGCAGAC GGACCGGGGG ACCGCACCGC 180
143 GCCGCGCCGG ACCGGGACTA TCTGCACCGG CCCAGTACT GCGACGCCCG CTTGCTCTG 240
145 GAGCAGATTT CCAAGGGGAA GGCTACTGGC CGGAAAGCGC CGTGTGGCT GAGAGCTGAAG 300
147 TTTCAGAGAC TCTTATTTAA ACTGGGTTGT TACATTCAA AGAACTGCGG CAAGTTTTTG 360
149 GTTGTGGGTC TCCTCATATT TGGGGCCTTC GCTGTGGGAT TAAAGGCAGC TAATCTCGAG 420
151 ACCAACGTGG AGGAGCTGTG GGTGGAAGTT GGTGGACGAG TGAGTCGAGA ATTAAATTAT 480

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153	ACCCGTCAGA	AGATAGGAGA	AGAGGCTATG	TTTAATCCTC	AACTCATGAT	ACAGACTCCA	540
155	AAAGAAGAAG	GCGCTAATGT	TCTGACCACA	GAGGCTCTCC	TGCAACACCT	GGACTCAGCA	600
157	CTCCAGGCCA	GTCGTGTGCA	CGTCTACATG	TATAACAGGC	AATGGAAGTT	GGAACATTTG	660
159	TGCTACAAAT	CAGGGGAAC	TATCACGGAG	ACAGGTTACA	TGGATCAGAT	AATAGAATAC	720
161	CTTTACCTT	GCTTAATCAT	TACACCTTTG	GACTGCTTCT	GGGAAGGGGC	AAAGCTACAG	780
163	TCCGGGACAG	CATACCTCCT	AGGTAAGCCT	CCTTTACGGT	GGACAAACTT	TGACCCCTTG	840
165	GAATTCCTAG	AAGAGTTAAA	GAAAATAAAC	TACCAAGTGG	ACAGCTGGGA	GGAAATGCTG	900
167	AATAAAGCCG	AAGTTGGCCA	TGGGTACATG	GACCGGCCTT	GCCTCAACCC	AGCCGACCCA	960
169	GATTGCCCTG	CCACAGCCCC	TAACAAAAAT	TCAACCAAAC	CTCTTGATGT	GGCCCTTGTT	1020
171	TTGAATGGTG	GATGTCAAGG	TTTATCCAGG	AAGTATATGC	ATTGGCAGGA	GGAGTTGATT	1080
173	GTGGGTGGTA	CCGTCAAGAA	TGCCACTGGA	AAACTTGTC	GCGCTCACGC	CCTGCAAACC	1140
175	ATGTTCCAGT	TAATGACTCC	CAAGCAAATG	TATGAACACT	TCAGGGGCTA	CGACTATGTC	1200
177	TCTCACATCA	ACTGGAATGA	AGACAGGGCA	GCCGCCATCC	TGGAGGCCTG	GCAGAGGACT	1260
179	TACGTGGAGG	TGGTTCATCA	AAGTGTGCGC	CCAAACTCCA	CTCAAAAGGT	GCTTCCCTTC	1320
181	ACAACCACGA	CCCTGGACGA	CATCCTAAAA	TCCTTCTCTG	ATGTCAGTGT	CATCCGAGTG	1380
183	GCCAGCGGCT	ACCTACTGAT	GCTTGCCTAT	GCGTGTCTTA	CCATGCTGCG	CTGGGACTGC	1440
185	TCCAAGTCCC	AGGGTGCCGT	GGGGCTGGCT	GGCGTCTGT	TGGTTGCGCT	GTCAGTGGCT	1500
187	GCAGGATTGG	GCCTCTGCTC	CTTGATTGGC	ATTTCTTTTA	ATGCTGCGAC	AACTCAGGTT	1560
189	TTGCCGTTTC	TTGCTCTTGG	TGTTGGTGTG	GATGATGTCT	TCCTCCTGGC	CCATGCATTC	1620
191	AGTGAAACAG	GACAGAATAA	GAGGATTCCA	TTTGAGGACA	GGACTGGGGA	GTGCCTCAAG	1680
193	CGCACCGGAG	CCAGCGTGGC	CCTCACCTCC	ATCAGCAATG	TCACCGCCTT	CCTCATGGCC	1740
195	GCATTGATCC	CTATCCCTGC	CCTGCGAGCG	TTCTCCCTCC	AGGCTGCTGT	GGTGGTGGTA	1800
197	TTCAATTTTG	CTATGTTTCT	GCTCATTTT	CCTGCAATTC	TCAGCATGGA	TTTATACAGA	1860
199	CGTGAGGACA	GAAGATTGGA	TATTTTCTGC	TGTTTCACAA	GCCCCTGTGT	CAGCAGGGTG	1920
201	ATTCAAAGTT	AGCCACAGGC	CTACACAGAG	CCTCACAGTA	ACACCCGGTA	CAGCCCCCCA	1980
203	CCCCCATACA	CCAGCCACAG	CTTCGCCCAC	GAAACCCATA	TCATCTATGCA	GTCCACCGTT	2040
205	CAGCTCCGCA	CAGAGTATGA	CCCTCACACG	CACGTGTACT	ACACCACCGC	CGAGCCACGC	2100
207	TCTGAGATCT	CTGTACAGCC	TGTTACCGTC	ACCCAGGACA	ACCTCAGCTG	TCAGAGTCCC	2160
209	GAGAGCACCA	GCTCTACCAG	GGACCTGCTC	TCCAGTTCT	CAGACTCCAG	CCTCCACTGC	2220
211	CTCGAGCCCC	CCTGCACCAA	GTGGACACTG	TCTTCGTTTG	CAGAGAAGCA	CTATGCTCCT	2280
213	TTCCTCCTGA	AACCCAAAGC	CAAGGTTGTG	GTAATCCTTC	TTTTCTGGG	CTTGCTGGGG	2340
215	GTGAGCCTTT	ATGGGACCAC	CCGAGTGAGA	GACGGGCTGG	ACCTCACGGA	CATTGTTCCC	2400
217	CGGGAAACCA	GAGAATATGA	CTTCATAGCT	GCCCAGTTCA	AGTACTTCTC	TTTCTACAAC	2460
219	ATGTATATAG	TCACCCAGAA	AGCAGACTAC	CCGAATATCC	AGCACCTACT	TTACGACCTT	2520
221	CATAAGAGTT	TCAGCAATGT	GAAGTATGTC	ATGCTGGAGG	AGAACAAGCA	ACTTCCCCAA	2580
223	ATGTGGCTGC	ACTACTTTAG	AGACTGGCTT	CAAGGACTTC	AGGATGCATT	TGACAGTGAC	2640
225	TGGGAAACTG	GGAGGATCAT	GCCAAACAAT	TATAAAAATG	GATCAGATGA	CGGGGTCCCT	2700
227	GCTTACAAAC	TCCTGGTGCA	GACTGGCAGC	CGAGACAAGC	CCATCGACAT	TAGTCAGTTG	2760
229	ACTAAACAGC	GTCTGGTAGA	CGCAGATGGC	ATCATTAATC	CGAGCGCTTT	CTACATCTAC	2820
231	CTGACCGCTT	GGGTACAGCA	CGACCTGTGA	GCTTACGCTG	CCTCCCAGGC	CAACATCCGG	2880
233	CCTCACCGGC	CGGAGTGGGT	CCATGACAAA	GCCGACTACA	TGCCAGAGAC	CAGGCTGAGA	2940
235	ATCCCAGCAG	CAGAGCCCAT	CGAGTACGCT	CAGTTCCCTT	TCTACCTCAA	CGGCCTACGA	3000
237	GACACCTCAG	ACTTTGTGGA	AGCCATAGAA	AAAGTGAGAG	TCATCTGTAA	CAACTATACG	3060
239	AGCCTGGGAC	TGTCCAGCTA	CCCCAATGGC	TACCCCTTCC	TGTTCTGGGA	GCAATACATC	3120
241	AGCCTGCGCC	ACTGGCTGCT	GCTATCCATC	AGCGTGGTGC	TGGCCTGCAC	GTTTCTAGTG	3180
243	TGCGCAGTCT	TCCTCCTGAA	CCCCTGGACG	GCCGGGATCA	TTGTCATGGT	CCTGGCTCTG	3240
245	ATGACCGTTG	AGCTCTTTGG	CATGATGGGC	CTCATTGGGA	TCAAGCTGAG	TGCTGTGCCT	3300
247	GTGGTCATCC	TGATTGCATC	TGTTGGCATC	GGAGTGGAGT	TCACCGTCCA	CGTGGCTTTG	3360
249	GCCTTTCTGA	CAGCCATTGG	GGACAAGAAC	CACAGGGGCTA	TGCTCGCTCT	GGAACACATG	3420

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```

251 TTTGCTCCCG TTCTGGACGG TGCTGTGTCC ACTCTGCTGG GTGTACTGAT GCTTGCAGGG 3480
253 TCCGAATTTG ATTTTCATTGT CAGATACTTC TTTGCCGTCC TGGCCATTCT CACCGTCTTG 3540
255 GGGGTTCTCA ATGGACTGGT TCTGCTGCCT GTCCTCTTAT CCTTCTTTGG ACCGTGTCCT 3600
257 GAGGTGTCTC CAGCCAATGG CCTAAACCGA CTGCCCCTC CTTGCGCTGA GCCGCTCCA 3660
259 AGTGTCGTCC GGTTCGCCGT GCCTCCTGGT CACACGAACA ATGGGTCTGA TTCCTCCGAC 3720
261 TCGGAGTACA GCTCTCAGAC CACGGTGTCT GGCATCAGTG AGGAGCTCAG GCAATACGAA 3780
263 GCACAGCAGG GTGCCGGAGG CCCTGCCCAC CAAGTGATTG TGGAAGCCAC AGAAAAACCT 3840
265 GTCTTTGCCC GGTCCACTGT GGTCCATCCG GACTCCAGAC ATCAGCCTCC CTTGACCCCT 3900
267 CGGCAACAGC CCCACCTGGA CTCTGGCTCC TTGTCCCCTG GACGGCAAGG CCAGCAGCCT 3960
269 CGAAGGGATC CCCCTAGAGA AGGCTTGCGG CCACCCCTT ACAGACCGCG CAGAGACGCT 4020
271 TTTGAAATTT CTACTGAAGG GCATTCTGGC CCTAGCAATA GGGACCGCTC AGGGCCCCGT 4080
273 GGGGCCCGTT CTCACAACCC TCGGAACCCA ACGTCCACCG CCATGGGCAG CTCTGTGCCC 4140
275 AGCTACTGCC AGCCCATCAC CACTGTGACG GCTTCTGCTT CGGTGACTGT TGCTGTGCAT 4200
277 CCCCCGCTG GACCTGGGCG CAACCCCGA GGGGGGCCCT GTCCAGGCTA TGAGAGCTAC 4260
279 CCTGAGACTG ATCACGGGGT ATTTGAGGAT CCTCATGTGC CTTTTCATGT CAGGTGTGAG 4320
281 AGGAGGGACT CAAAGGTGGA GGTCATAGAG CTACAGGACG TGAATGTGA GGAGAGGCCG 4380
283 TGGGGGAGCA GCTCCAACCT AGGGTAATTA AAATCTGAAG CAAAGAGGCC AAAGATTGGA 4440
285 AAGCCCCGCC CCCACCTCTT TCCAGAACTG CTTGAAGAGA ACTGCTTGA ATTATGGGAA 4500
287 GGCAGTTCAT TGTTACTGTA ACTGATTGTA TTATTKKGTG AAATATTTCT ATAAATATTT 4560
289 AARAGGTGTA CACATGTAAT ATACATGGAA ATGCTGTACA GTCTATTTCC TGGGGCCTCT 4620
291 CCACTCCTGC CCCAGAGTGG GGAGACCACA GGGGCCCTTT CCCCTGTGTA CATTGGTCTC 4680
293 TGTGCCACAA CCAAGCTTAA CTTAGTTTTA AAAAAATCT CCCAGCATAT GTCGCTGCTG 4740
295 CTTAAATATT GTATAATTTA CTTGTATAAT TCTATGCAA TATTGCTTAT GTAATAGGAT 4800
297 TATTTGTAAA GGTTCCTGTT TAAATATTT TAAATTTGCA TATCACAACC CTGTGGTAGG 4860
299 ATGAATTGTT ACTGTAACT TTTGAACACG CTATGCGTGG TAATTGTTA ACGAGCAGAC 4920
301 ATGAAGAAAA CAGGTAAATC CCAGTGCTT CTCTAGGGGT AGTTGTATAT GGTTCCGATG 4980
303 GGTGGATGTG TGTGTGCATG TGACTTTCCA ATGTACTGTA TTGTGGTTTG TTGTTGTTGT 5040
305 TGCTGTTGTT GTTCATTTG GTGTTTTTG TTGCTTTGTA TGATCTTAGC TCTGGCCTAG 5100
307 GTGGGCTGGG AAGGTCCAGG TCTTTTCTG TCGTGATGCT GGTGGAAAGG TGACCCCAAT 5160
309 CATCTGTCCT ATTCTCTGGG ACTATTC
311 (2) INFORMATION FOR SEQ ID NO: 4:
313 (i) SEQUENCE CHARACTERISTICS:
314 (A) LENGTH: 1311 amino acids
315 (B) TYPE: amino acid
316 (C) STRANDEDNESS: single
317 (D) TOPOLOGY: linear
319 (ii) MOLECULE TYPE: protein
324 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
326 Met Val Ala Pro Asp Ser Glu Ala Pro Ser Asn Pro Arg Ile Thr Ala
327 1 5 10 15
329 Ala His Glu Ser Pro Cys Ala Thr Glu Ala Arg His Ser Ala Asp Leu
330 20 25 30
332 Tyr Ile Arg Thr Ser Trp Val Asp Ala Ala Leu Ala Leu Ser Glu Leu
333 35 40 45
335 Glu Lys Gly Asn Ile Glu Gly Gly Arg Thr Ser Leu Trp Ile Arg Ala
336 50 55 60
338 Trp Leu Gln Glu Gln Leu Phe Ile Leu Gly Cys Phe Leu Gln Gly Asp
339 65 70 75 80
341 Ala Gly Lys Val Leu Phe Val Ala Ile Leu Val Leu Ser Thr Phe Cys

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342          85          90          95
344  Val Gly Leu Lys Ser Ala Gln Ile His Thr Arg Val Asp Gln Leu Trp
345          100          105          110
347  Val Gln Glu Gly Gly Arg Leu Glu Ala Glu Leu Lys Tyr Thr Ala Gln
348          115          120          125
350  Ala Leu Gly Glu Ala Asp Ser Ser Thr His Gln Leu Val Ile Gln Thr
351          130          135          140
353  Ala Lys Asp Pro Asp Val Ser Leu Leu His Pro Gly Ala Leu Leu Glu
354          145          150          155          160
356  His Leu Lys Val Val His Ala Ala Thr Arg Val Thr Val His Met Tyr
357          165          170          175
359  Asp Ile Glu Trp Arg Leu Lys Asp Leu Cys Tyr Ser Pro Ser Ile Pro
360          180          185          190
362  Asp Phe Glu Gly Tyr His His Ile Glu Ser Ile Ile Asp Asn Val Ile
363          195          200          205
365  Pro Cys Ala Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly Ser Lys
366          210          215          220
368  Leu Leu Gly Pro Asp Tyr Pro Ile Tyr Val Pro His Leu Lys His Lys
369          225          230          235          240
371  Leu Gln Trp Thr His Leu Asn Pro Leu Glu Val Val Glu Glu Val Lys
372          245          250          255
374  Lys Leu Lys Phe Gln Phe Pro Leu Ser Thr Thr Ile Glu Ala Tyr Met Lys
375          260          265          270
377  Arg Ala Gly Ile Thr Ser Ala Tyr Met Lys Lys Pro Cys Leu Asp Pro
378          275          280          285
380  Thr Asp Pro His Cys Pro Ala Thr Ala Pro Asn Lys Lys Ser Gly His
381          290          295          300
383  Ile Pro Asp Val Ala Ala Glu Leu Ser His Gly Cys Tyr Gly Phe Ala
384          305          310          315          320
386  Ala Ala Tyr Met His Trp Pro Glu Gln Leu Ile Val Gly Gly Ala Thr
387          325          330          335
W--> 389  Arg Asn Ser Thr Ser Ala Leu Arg Lys Ala Arg Xaa Leu Gln Thr Val
390          340          345          350
392  Val Gln Leu Met Gly Glu Arg Glu Met Tyr Glu Tyr Trp Ala Asp His
393          355          360          365
395  Tyr Lys Val His Gln Ile Gly Trp Asn Gln Glu Lys Ala Ala Ala Val
396          370          375          380
398  Leu Asp Ala Trp Gln Arg Lys Phe Ala Ala Glu Val Arg Lys Ile Thr
399          385          390          395          400
401  Thr Ser Gly Ser Val Ser Ser Ala Tyr Ser Phe Tyr Pro Phe Ser Thr
402          405          410          415
404  Ser Thr Leu Asn Asp Ile Leu Gly Lys Phe Ser Glu Val Ser Leu Lys
405          420          425          430
407  Asn Ile Ile Leu Gly Tyr Met Phe Met Leu Ile Tyr Val Ala Val Thr
408          435          440          445
410  Leu Ile Gln Trp Arg Asp Pro Ile Arg Ser Gln Ala Gly Val Gly Ile
411          450          455          460
413  Ala Gly Val Leu Leu Leu Ser Ile Thr Val Ala Ala Gly Leu Gly Phe
414          465          470          475          480

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 4,5,7,8,10,11,23,34,35,36,39,40,41,45,51,52,57,61,71,75,77
Seq#:1; N Pos. 87,88,89,91,92,96,97,100,104,106,109,111,113,117,120,126,149
Seq#:1; N Pos. 151,153,154,157,178,187,189,191,211,214,310,608,704,708,712
Seq#:1; N Pos. 714,729,732
Seq#:2; Xaa Pos.1,9,12,13,14,20
Seq#:4; Xaa Pos.348,908
Seq#:7; N Pos. 114,225,261
Seq#:8; Xaa Pos.75,87
Seq#:14; N Pos. 16,25
Seq#:15; N Pos. 24
Seq#:16; N Pos. 13,16
Seq#:17; N Pos. 20

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09754032.RAW.txt

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:34 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
M:341 Repeated in SeqNo=2
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:336
M:341 Repeated in SeqNo=4
L:1047 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:64
M:341 Repeated in SeqNo=8